

GAP of: 0964DP54725 check: 3361 from: 1 to: 363

WPDEF Case 0964D Rad23 SwissProt P54725 Human Rad23A

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P54725. UV excision repai. . .[gi:1709983] BLink, Domains, Links

LOCUS P54725 363 aa linear PRI 15-

SEP-2003

DEFINITION UV excision repair protein RAD23 homolog A (HHR23A).

ACCESSION P54725 . . .

to: 0964sid4 check: 9188 from: 1 to: 368

WPDEF Case 0964 Rad23 SEQ ID NO: 4 corn

Case 0964 Rad23 SEQ ID NO: 4 corn

Symbol comparison table: blosum62.cmp CompCheck: 1102

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. Proc. Natl. Acad.

Sci. USA 89: 10915-10919.

Gap Weight: 8 Average Match: 2.778  
Length Weight: 2 Average Mismatch: -2.248

Quality: 537 Length: 393  
Ratio: 1.479 Gaps: 8  
Percent Similarity: 52.959 Percent Identity: 38.757

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 2  
. = 1

0964DP54725 x 0964sid4 October 28, 2003 11:27 ..

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      .      .      .      .      .
1 mavtitlktlqqqtfkirmepdetvkvkkekiaekgrdafpvagqkliy 50
  . :|.|||. |.||.:|.:|: .|. || .|:|.:.| | ||:
1 ..MKLTVKTLKGTHFEIRVQPNDTIMAVKKNIEEIQGKDSYPWGQQLLIF 48
      .      .      .      .      .
51 agkilsddvpirdyrideknfvvmvktkagqgtsappeasptaapess 100
  ||:| |: : : :.:| |.||||. | | | |
49 NGKVLKDESTLEENKVNEDGFLVVMLSKGKTSGSTGT.....SS 87
      .      .      .      .      .
101 tsfppaptsgmshpppaaredkspseesapttspesvsgsvpssgssgre 150
  . |. . | |.: | |. || . |..
88 SQHSNTPATRQAPPLEAPQQAPQPPVAPITTSQPEGLPAQAPNT.....H 132
      .      .      .      .      .
151 edaastlvtgseyetmlteismg...yerervvaalrasynnpgravey 197
  :.|||| |..| :|.: :.:| || :.:.:| ||||.|||| ||||
133 DNAASNLLSGRNVDTIINQLMEMGGGSWDKDKVQRALRAAYNNPERAVEY 182
      .      .      .      .      .
198 lltgip.....gspepehgsvqesqvseqpate..... 225
  |.|||| |. : |. .| | |
183 LYSGIPVTAEIAVPIGGQGANTTDRAPTGEAGLSGIPNTAPLDLFPQGAS 232
      .      .      .      .      .

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226 ....aagenpleflrdqpqfqnmrqviqqnpallpallqqlgqenpqllq 271  
 || ||:||||. |||| .|:..: || :| :| :| .:||||:|.

233 NAGGGAGGGPLDFLRNNPQFQAVREMVHTNPQILQPMLVELSKQNPQILR 282

272 qisrhqeqfiqmlnep.pgela disdvegevgageeapqmnyiqvtpqe 320  
 | . :|:|:|||| | | | | :| | . | |||:|

283 LIEENHDEFLQLLNEPFEGGEGDFLDQPEE.....DEMP..HAISVTPEE 325

321 keaierlkalgfpeslviqayfaceknenlaanflsqnfdde 363  
 .||| ||..:|| . ||:|: ||:| ||||:|| :::

326 QEAIGRLESMGFDRARVIEAFLACDRNEELAANYLLEHAGEED 368